



SEQUENCE LISTING

<110> THE UNITED STATES OF AMERICA represented by THE SE

<120> AIB1, A novel steroid receptor co-activator

<130> 49944

<140> PCT/US98/12689

<141> 1998-06-17

<150> 60/049,728

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<170> PatentIn Ver. 2.0

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35 40 45
Asp Arg Lys Asp Phe Leu Lys Asn Leu Pro Lys Ser Thr Val Asn Gly
50 55 60
Val Ser Trp Thr Asn Glu Thr Gln Arg Gln Lys Ser His Thr Phe Asn
65 70 75 80
Cys Arg Met Leu Met Lys Thr Pro His Asp Ile Leu Glu Asp Ile Asn
85 90 95
Ala Ser Pro Glu Met Arg Gln Arg Tyr Glu Thr Met Gln Cys Phe Ala
100 105 110
Leu Ser Gln Pro Arg Ala Met Met Glu Glu Gly Glu Asp Leu Gln Ser
115 120 125
Cys Met Ile Cys Val Ala Arg Arg Ile Thr Thr Gly Glu Arg Thr Phe
130 135 140
Pro Ser Asn Pro Glu Ser Phe Ile Thr Arg His Asp Leu Ser Gly Lys
145 150 155 160
Val Val Asn Ile Asp Thr Asn Ser Leu Arg Ser Ser Met Arg Pro Gly
165 170 175
Phe Glu Asp Ile Ile Arg Arg Cys Ile Gln

180

185

<210> 3
 <211> 73
 <212> PRT
 <213> Homo sapiens

<400> 3
 Arg Lys Arg Lys Leu Pro Cys Asp Thr Pro Gly Gln Gly Leu Thr Cys
 1 5 10 15
 Ser Gly Glu Lys Arg Arg Arg Glu Gln Glu Ser Lys Tyr Ile Glu Glu
 20 25 30
 Leu Ala Glu Leu Ile Ser Ala Asn Leu Ser Asp Ile Asp Asn Phe Asn
 35 40 45
 Val Lys Pro Asp Lys Cys Ala Ile Leu Lys Glu Thr Val Arg Gln Ile
 50 55 60
 Arg Gln Ile Lys Glu Gln Gly Lys Thr
 65 70

<210> 4
 <211> 1420
 <212> PRT
 <213> Homo sapiens

<400> 4
 Met Ser Gly Leu Gly Glu Asn Leu Asp Pro Leu Ala Ser Asp Ser Arg
 1 5 10 15
 Lys Arg Lys Leu Pro Cys Asp Thr Pro Gly Gln Gly Leu Thr Cys Ser
 20 25 30
 Gly Glu Lys Arg Arg Arg Glu Gln Glu Ser Lys Tyr Ile Glu Glu Leu
 35 40 45
 Ala Glu Leu Ile Ser Ala Asn Leu Ser Asp Ile Asp Asn Phe Asn Val
 50 55 60
 Lys Pro Asp Lys Cys Ala Ile Leu Lys Glu Thr Val Arg Gln Ile Arg
 65 70 75 80
 Gln Ile Lys Glu Gln Gly Lys Thr Ile Ser Asn Asp Asp Asp Val Gln
 85 90 95
 Lys Ala Asp Val Ser Ser Thr Gly Gln Gly Val Ile Asp Lys Asp Ser
 100 105 110
 Leu Gly Pro Leu Leu Leu Gln Ala Leu Asp Gly Phe Leu Phe Val Val
 115 120 125
 Asn Arg Asp Gly Asn Ile Val Phe Val Ser Glu Asn Val Thr Gln Tyr
 130 135 140

Leu Gln Tyr Lys Gln Glu Asp Leu Val Asn Thr Ser Val Tyr Asn Ile
 145 150 155 160
 Leu His Glu Glu Asp Arg Lys Asp Phe Leu Lys Asn Leu Pro Lys Ser
 165 170 175
 Thr Val Asn Gly Val Ser Trp Thr Asn Glu Thr Gln Arg Gln Lys Ser
 180 185 190
 His Thr Phe Asn Cys Arg Met Leu Met Lys Thr Pro His Asp Ile Leu
 195 200 205
 Glu Asp Ile Asn Ala Ser Pro Glu Met Arg Gln Arg Tyr Glu Thr Met
 210 215 220
 Gln Cys Phe Ala Leu Ser Gln Pro Arg Ala Met Met Glu Glu Gly Glu
 225 230 235 240
 Asp Leu Gln Ser Cys Met Ile Cys Val Ala Arg Arg Ile Thr Thr Gly
 245 250 255
 Glu Arg Thr Phe Pro Ser Asn Pro Glu Ser Phe Ile Thr Arg His Asp
 260 265 270
 Leu Ser Gly Lys Val Val Asn Ile Asp Thr Asn Ser Leu Arg Ser Ser
 275 280 285
 Met Arg Pro Gly Phe Glu Asp Ile Ile Arg Arg Cys Ile Gln Arg Phe
 290 295 300
 Phe Ser Leu Asn Asp Gly Gln Ser Trp Ser Gln Lys Arg His Tyr Gln
 305 310 315 320
 Glu Ala Tyr Leu Asn Gly His Ala Glu Thr Pro Val Tyr Arg Phe Ser
 325 330 335
 Leu Ala Asp Gly Thr Ile Val Thr Ala Gln Thr Lys Ser Lys Leu Phe
 340 345 350
 Arg Asn Pro Val Thr Asn Asp Arg His Gly Phe Val Ser Thr His Phe
 355 360 365
 Leu Gln Arg Glu Gln Asn Gly Tyr Arg Pro Asn Pro Asn Pro Val Gly
 370 375 380
 Gln Gly Ile Arg Pro Pro Met Ala Gly Cys Asn Ser Ser Val Gly Gly
 385 390 395 400
 Met Ser Met Ser Pro Asn Gln Gly Leu Gln Met Pro Ser Ser Arg Ala
 405 410 415
 Tyr Gly Leu Ala Asp Pro Ser Thr Thr Gly Gln Met Ser Gly Ala Arg
 420 425 430
 Tyr Gly Gly Ser Ser Asn Ile Ala Ser Leu Thr Pro Gly Pro Gly Met
 435 440 445

Gln Ser Pro Ser Ser Tyr Gln Asn Asn Asn Tyr Gly Leu Asn Met Ser
 450 455 460
 Ser Pro Pro His Gly Ser Pro Gly Leu Ala Pro Asn Gln Gln Asn Ile
 465 470 475 480
 Met Ile Ser Pro Arg Asn Arg Gly Ser Pro Lys Ile Ala Ser His Gln
 485 490 495
 Phe Ser Pro Val Ala Gly Val His Ser Pro Met Ala Ser Ser Gly Asn
 500 505 510
 Thr Gly Asn His Ser Phe Ser Ser Ser Ser Leu Ser Ala Leu Gln Ala
 515 520 525
 Ile Ser Glu Gly Val Gly Thr Ser Leu Leu Ser Thr Leu Ser Ser Pro
 530 535 540
 Gly Pro Lys Leu Asp Asn Ser Pro Asn Met Asn Ile Thr Gln Pro Ser
 545 550 555 560
 Lys Val Ser Asn Gln Asp Ser Lys Ser Pro Leu Gly Phe Tyr Cys Asp
 565 570 575
 Gln Asn Pro Val Glu Ser Ser Met Cys Gln Ser Asn Ser Arg Asp His
 580 585 590
 Leu Ser Asp Lys Glu Ser Lys Glu Ser Ser Val Glu Gly Ala Glu Asn
 595 600 605
 Gln Arg Gly Pro Leu Glu Ser Lys Gly His Lys Lys Leu Leu Gln Leu
 610 615 620
 Leu Thr Cys Ser Ser Asp Asp Arg Gly His Ser Ser Leu Thr Asn Ser
 625 630 635 640
 Pro Leu Asp Ser Ser Cys Lys Glu Ser Ser Val Ser Val Thr Ser Pro
 645 650 655
 Ser Gly Val Ser Ser Ser Thr Ser Gly Gly Val Ser Ser Thr Ser Asn
 660 665 670
 Met His Gly Ser Leu Leu Gln Glu Lys His Arg Ile Leu His Lys Leu
 675 680 685
 Leu Gln Asn Gly Asn Ser Pro Ala Glu Val Ala Lys Ile Thr Ala Glu
 690 695 700
 Ala Thr Gly Lys Asp Thr Ser Ser Ile Thr Ser Cys Gly Asp Gly Asn
 705 710 715 720
 Val Val Lys Gln Glu Gln Leu Ser Pro Lys Lys Lys Glu Asn Asn Ala
 725 730 735
 Leu Leu Arg Tyr Leu Leu Asp Arg Asp Asp Pro Ser Asp Ala Leu Ser
 740 745 750

Lys	Glu	Leu	Gln	Pro	Gln	Val	Glu	Gly	Val	Asp	Asn	Lys	Met	Ser	Gln	755	760	765
Cys	Thr	Ser	Ser	Thr	Ile	Pro	Ser	Ser	Ser	Gln	Glu	Lys	Asp	Pro	Lys	770	775	780
Ile	Lys	Thr	Glu	Thr	Ser	Glu	Glu	Gly	Ser	Gly	Asp	Leu	Asp	Asn	Leu	785	790	795
Asp	Ala	Ile	Leu	Gly	Asp	Leu	Thr	Ser	Ser	Asp	Phe	Tyr	Asn	Asn	Ser	805	810	815
Ile	Ser	Ser	Asn	Gly	Ser	His	Leu	Gly	Thr	Lys	Gln	Gln	Val	Phe	Gln	820	825	830
Gly	Thr	Asn	Ser	Leu	Gly	Leu	Lys	Ser	Ser	Gln	Ser	Val	Gln	Ser	Ile	835	840	845
Arg	Pro	Pro	Tyr	Asn	Arg	Ala	Val	Ser	Leu	Asp	Ser	Pro	Val	Ser	Val	850	855	860
Gly	Ser	Ser	Pro	Pro	Val	Lys	Asn	Ile	Ser	Ala	Phe	Pro	Met	Leu	Pro	865	870	875
Lys	Gln	Pro	Met	Leu	Gly	Gly	Asn	Pro	Arg	Met	Met	Asp	Ser	Gln	Glu	885	890	895
Asn	Tyr	Gly	Ser	Ser	Met	Gly	Gly	Pro	Asn	Arg	Asn	Val	Thr	Val	Thr	900	905	910
Gln	Thr	Pro	Ser	Ser	Gly	Asp	Trp	Gly	Leu	Pro	Asn	Ser	Lys	Ala	Gly	915	920	925
Arg	Met	Glu	Pro	Met	Asn	Ser	Asn	Ser	Met	Gly	Arg	Pro	Gly	Gly	Asp	930	935	940
Tyr	Asn	Thr	Ser	Leu	Pro	Arg	Pro	Ala	Leu	Gly	Gly	Ser	Ile	Pro	Thr	945	950	955
Leu	Pro	Leu	Arg	Ser	Asn	Ser	Ile	Pro	Gly	Ala	Arg	Pro	Val	Leu	Gln	965	970	975
Gln	Gln	Gln	Gln	Met	Leu	Gln	Met	Arg	Pro	Gly	Glu	Ile	Pro	Met	Gly	980	985	990
Met	Gly	Ala	Asn	Pro	Tyr	Gly	Gln	Ala	Ala	Ala	Ser	Asn	Gln	Leu	Gly	995	1000	1005
Ser	Trp	Pro	Asp	Gly	Met	Leu	Ser	Met	Glu	Gln	Val	Ser	His	Gly	Thr	1010	1015	1020
Gln	Asn	Arg	Pro	Leu	Leu	Arg	Asn	Ser	Leu	Asp	Asp	Leu	Val	Gly	Pro	1025	1030	1035
Pro	Ser	Asn	Leu	Glu	Gly	Gln	Ser	Asp	Glu	Arg	Ala	Leu	Leu	Asp	Gln	1045	1050	1055

Leu His Thr Leu Leu Ser Asn Thr Asp Ala Thr Gly Leu Glu Glu Ile
 1060 1065 1070
 Asp Arg Ala Leu Gly Ile Pro Glu Leu Val Asn Gln Gly Gln Ala Leu
 1075 1080 1085
 Glu Pro Lys Gln Asp Ala Phe Gln Gly Gln Glu Ala Ala Val Met Met
 1090 1095 1100
 Asp Gln Lys Ala Gly Leu Tyr Gly Gln Thr Tyr Pro Ala Gln Gly Pro
 1105 1110 1115 1120
 Pro Met Gln Gly Gly Phe His Leu Gln Gly Gln Ser Pro Ser Phe Asn
 1125 1130 1135
 Ser Met Met Asn Gln Met Asn Gln Gln Gly Asn Phe Pro Leu Gln Gly
 1140 1145 1150
 Met His Pro Arg Ala Asn Ile Met Arg Pro Arg Thr Asn Thr Pro Lys
 1155 1160 1165
 Gln Leu Arg Met Gln Leu Gln Gln Arg Leu Gln Gly Gln Gln Phe Leu
 1170 1175 1180
 Asn Gln Ser Arg Gln Ala Leu Glu Leu Lys Met Glu Asn Pro Thr Ala
 1185 1190 1195 1200
 Gly Gly Ala Ala Val Met Arg Pro Met Met Gln Pro Gln Gln Gly Phe
 1205 1210 1215
 Leu Asn Ala Gln Met Val Ala Gln Arg Ser Arg Glu Leu Leu Ser His
 1220 1225 1230
 His Phe Arg Gln Gln Arg Val Ala Met Met Met Gln Gln Gln Gln
 1235 1240 1245
 Gln Gln Gln Gln Gln Gln Gln Gln Gln Gln Gln Gln Gln Gln Gln
 1250 1255 1260
 Gln Gln Gln Gln Gln Gln Gln Gln Thr Gln Ala Phe Ser Pro Pro Pro
 1265 1270 1275 1280
 Asn Val Thr Ala Ser Pro Ser Met Asp Gly Leu Leu Ala Gly Pro Thr
 1285 1290 1295
 Met Pro Gln Ala Pro Pro Gln Gln Phe Pro Tyr Gln Pro Asn Tyr Gly
 1300 1305 1310
 Met Gly Gln Gln Pro Asp Pro Ala Phe Gly Arg Val Ser Ser Pro Pro
 1315 1320 1325
 Asn Ala Met Met Ser Ser Arg Met Gly Pro Ser Gln Asn Pro Met Met
 1330 1335 1340
 Gln His Pro Gln Ala Ala Ser Ile Tyr Gln Ser Ser Glu Met Lys Gly
 1345 1350 1355 1360

Trp Pro Ser Gly Asn Leu Ala Arg Asn Ser Ser Phe Ser Gln Gln Gln
1365 1370 1375

Phe Ala His Gln Gly Asn Pro Ala Val Tyr Ser Met Val His Met Asn
1380 1385 1390

Gly Ser Ser Gly His Met Gly Gln Met Asn Met Asn Pro Met Pro Met
1395 1400 1405

Ser Gly Met Pro Met Gly Pro Asp Gln Lys Tyr Cys
1410 1415 1420

<210> 5

<211> 22

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:PRIMER N8F1

<400> 5

tcatcacttc cgacaacaga gg

22

<210> 6

<211> 20

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: forward primer
designed from the 5' sequence of pCMVSPORT-B11,
PM-U2

<400> 6

ccagaaacgt cactatcaag

20

<210> 7

<211> 19

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: reverse primer
designed from the 5' sequence of pCMVSPORT-B11,
PM-U2

<400> 7

ttactggaac ccccatacc

19

<210> 8

<211> 951

<212> PRT

40

<213> Homo sapiens

<400> 8

Cys	Ile	Gln	Arg	Phe	Phe	Ser	Leu	Asn	Asp	Gly	Gln	Ser	Trp	Ser	Gln	
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Lys	Arg	His	Tyr	Gln	Glu	Ala	Tyr	Leu	Asn	Gly	His	Ala	Glu	Thr	Pro	
			20					25					30			
Val	Tyr	Arg	Phe	Ser	Leu	Ala	Asp	Gly	Thr	Ile	Val	Thr	Ala	Gln	Thr	
		35					40					45				
Lys	Ser	Lys	Leu	Phe	Arg	Asn	Pro	Val	Thr	Asn	Asp	Arg	His	Gly	Phe	
	50					55					60					
Val	Ser	Thr	His	Phe	Leu	Gln	Arg	Glu	Gln	Asn	Gly	Tyr	Arg	Pro	Asn	
	65				70					75					80	
Pro	Asn	Pro	Val	Gly	Gln	Gly	Ile	Arg	Pro	Pro	Met	Ala	Gly	Cys	Asn	
				85					90					95		
Ser	Ser	Val	Gly	Gly	Met	Ser	Met	Ser	Pro	Asn	Gln	Gly	Leu	Gln	Met	
			100					105					110			
Pro	Ser	Ser	Arg	Ala	Tyr	Gly	Leu	Ala	Asp	Pro	Ser	Thr	Thr	Gly	Gln	
		115					120					125				
Met	Ser	Gly	Ala	Arg	Tyr	Gly	Gly	Ser	Ser	Asn	Ile	Ala	Ser	Leu	Thr	
	130					135					140					
Pro	Gly	Pro	Gly	Met	Gln	Ser	Pro	Ser	Ser	Tyr	Gln	Asn	Asn	Asn	Tyr	
	145				150					155					160	
Gly	Leu	Asn	Met	Ser	Ser	Pro	Pro	His	Gly	Ser	Pro	Gly	Leu	Ala	Pro	
			165						170					175		
Asn	Gln	Gln	Asn	Ile	Met	Ile	Ser	Pro	Arg	Asn	Arg	Gly	Ser	Pro	Lys	
		180						185					190			
Ile	Ala	Ser	His	Gln	Phe	Ser	Pro	Val	Ala	Gly	Val	His	Ser	Pro	Met	
		195					200					205				
Ala	Ser	Ser	Gly	Asn	Thr	Gly	Asn	His	Ser	Phe	Ser	Ser	Ser	Ser	Leu	
	210					215					220					
Ser	Ala	Leu	Gln	Ala	Ile	Ser	Glu	Gly	Val	Gly	Thr	Ser	Leu	Leu	Ser	
	225				230					235					240	
Thr	Leu	Ser	Ser	Pro	Gly	Pro	Lys	Leu	Asp	Asn	Ser	Pro	Asn	Met	Asn	
			245						250					255		
Ile	Thr	Gln	Pro	Ser	Lys	Val	Ser	Asn	Gln	Asp	Ser	Lys	Ser	Pro	Leu	
		260						265					270			
Gly	Phe	Tyr	Cys	Asp	Gln	Asn	Pro	Val	Glu	Ser	Ser	Met	Cys	Gln	Ser	
		275					280					285				

Asn	Ser	Arg	Asp	His	Leu	Ser	Asp	Lys	Glu	Ser	Lys	Glu	Ser	Ser	Val
290						295					300				
Glu	Gly	Ala	Glu	Asn	Gln	Arg	Gly	Pro	Leu	Glu	Ser	Lys	Gly	His	Lys
305					310					315					320
Lys	Leu	Leu	Gln	Leu	Leu	Thr	Cys	Ser	Ser	Asp	Asp	Arg	Gly	His	Ser
			325						330					335	
Ser	Leu	Thr	Asn	Ser	Pro	Leu	Asp	Ser	Ser	Cys	Lys	Glu	Ser	Ser	Val
			340					345					350		
Ser	Val	Thr	Ser	Pro	Ser	Gly	Val	Ser	Ser	Ser	Thr	Ser	Gly	Gly	Val
		355					360					365			
Ser	Ser	Thr	Ser	Asn	Met	His	Gly	Ser	Leu	Leu	Gln	Glu	Lys	His	Arg
	370					375					380				
Ile	Leu	His	Lys	Leu	Leu	Gln	Asn	Gly	Asn	Ser	Pro	Ala	Glu	Val	Ala
385					390					395					400
Lys	Ile	Thr	Ala	Glu	Ala	Thr	Gly	Lys	Asp	Thr	Ser	Ser	Ile	Thr	Ser
			405						410					415	
Cys	Gly	Asp	Gly	Asn	Val	Val	Lys	Gln	Glu	Gln	Leu	Ser	Pro	Lys	Lys
			420					425					430		
Lys	Glu	Asn	Asn	Ala	Leu	Leu	Arg	Tyr	Leu	Leu	Asp	Arg	Asp	Asp	Pro
		435					440					445			
Ser	Asp	Ala	Leu	Ser	Lys	Glu	Leu	Gln	Pro	Gln	Val	Glu	Gly	Val	Asp
	450					455					460				
Asn	Lys	Met	Ser	Gln	Cys	Thr	Ser	Ser	Thr	Ile	Pro	Ser	Ser	Ser	Gln
465					470					475					480
Glu	Lys	Asp	Pro	Lys	Ile	Lys	Thr	Glu	Thr	Ser	Glu	Glu	Gly	Ser	Gly
			485						490					495	
Asp	Leu	Asp	Asn	Leu	Asp	Ala	Ile	Leu	Gly	Asp	Leu	Thr	Ser	Ser	Asp
			500					505					510		
Phe	Tyr	Asn	Asn	Ser	Ile	Ser	Ser	Asn	Gly	Ser	His	Leu	Gly	Thr	Lys
		515					520					525			
Gln	Gln	Val	Phe	Gln	Gly	Thr	Asn	Ser	Leu	Gly	Leu	Lys	Ser	Ser	Gln
	530					535					540				
Ser	Val	Gln	Ser	Ile	Arg	Pro	Pro	Tyr	Asn	Arg	Ala	Val	Ser	Leu	Asp
545					550					555					560
Ser	Pro	Val	Ser	Val	Gly	Ser	Ser	Pro	Pro	Val	Lys	Asn	Ile	Ser	Ala
				565					570					575	
Phe	Pro	Met	Leu	Pro	Lys	Gln	Pro	Met	Leu	Gly	Gly	Asn	Pro	Arg	Met
			580					585					590		

Met Asp Ser Gln Glu Asn Tyr Gly Ser Ser Met Gly Gly Pro Asn Arg
 595 600 605
 Asn Val Thr Val Thr Gln Thr Pro Ser Ser Gly Asp Trp Gly Leu Pro
 610 615 620
 Asn Ser Lys Ala Gly Arg Met Glu Pro Met Asn Ser Asn Ser Met Gly
 625 630 635 640
 Arg Pro Gly Gly Asp Tyr Asn Thr Ser Leu Pro Arg Pro Ala Leu Gly
 645 650 655
 Gly Ser Ile Pro Thr Leu Pro Leu Arg Ser Asn Ser Ile Pro Gly Ala
 660 665 670
 Arg Pro Val Leu Gln Gln Gln Gln Met Leu Gln Met Arg Pro Gly
 675 680 685
 Glu Ile Pro Met Gly Met Gly Ala Asn Pro Tyr Gly Gln Ala Ala Ala
 690 695 700
 Ser Asn Gln Leu Gly Ser Trp Pro Asp Gly Met Leu Ser Met Glu Gln
 705 710 715 720
 Val Ser His Gly Thr Gln Asn Arg Pro Leu Leu Arg Asn Ser Leu Asp
 725 730 735
 Asp Leu Val Gly Pro Pro Ser Asn Leu Glu Gly Gln Ser Asp Glu Arg
 740 745 750
 Ala Leu Leu Asp Gln Leu His Thr Leu Leu Ser Asn Thr Asp Ala Thr
 755 760 765
 Gly Leu Glu Glu Ile Asp Arg Ala Leu Gly Ile Pro Glu Leu Val Asn
 770 775 780
 Gln Gly Gln Ala Leu Glu Pro Lys Gln Asp Ala Phe Gln Gly Gln Glu
 785 790 795 800
 Ala Ala Val Met Met Asp Gln Lys Ala Gly Leu Tyr Gly Gln Thr Tyr
 805 810 815
 Pro Ala Gln Gly Pro Pro Met Gln Gly Gly Phe His Leu Gln Gly Gln
 820 825 830
 Ser Pro Ser Phe Asn Ser Met Met Asn Gln Met Asn Gln Gln Gly Asn
 835 840 845
 Phe Pro Leu Gln Gly Met His Pro Arg Ala Asn Ile Met Arg Pro Arg
 850 855 860
 Thr Asn Thr Pro Lys Gln Leu Arg Met Gln Leu Gln Gln Arg Leu Gln
 865 870 875 880
 Gly Gln Gln Phe Leu Asn Gln Ser Arg Gln Ala Leu Glu Leu Lys Met
 885 890 895

ccg ctt tta cta cag gca ctg gat ggt ttc ctg ttt gtg gtg aat cga	502
Pro Leu Leu Leu Gln Ala Leu Asp Gly Phe Leu Phe Val Val Asn Arg	
120 125 130	
gat gga aac att gta ttc gtg tca gaa aat gtc aca cag tat ctg cag	550
Asp Gly Asn Ile Val Phe Val Ser Glu Asn Val Thr Gln Tyr Leu Gln	
135 140 145	
tac aag cag gag gac ctg gtt aac aca agt gtc tac agc atc tta cat	598
Tyr Lys Gln Glu Asp Leu Val Asn Thr Ser Val Tyr Ser Ile Leu His	
150 155 160	
gag caa gac cgg aag gat ttt ctt aaa cac tta cca aaa tcc aca gtt	646
Glu Gln Asp Arg Lys Asp Phe Leu Lys His Leu Pro Lys Ser Thr Val	
165 170 175	
aat gga gtt tct tgg act aat gag aac cag aga caa aaa agc cat aca	694
Asn Gly Val Ser Trp Thr Asn Glu Asn Gln Arg Gln Lys Ser His Thr	
180 185 190 195	
ttt aat tgt cgt atg ttg atg aaa aca cac gac att ttg gaa gac gtg	742
Phe Asn Cys Arg Met Leu Met Lys Thr His Asp Ile Leu Glu Asp Val	
200 205 210	
aat gcc agt ccc gaa aca cgc cag aga tat gaa aca atg cag tgc ttt	790
Asn Ala Ser Pro Glu Thr Arg Gln Arg Tyr Glu Thr Met Gln Cys Phe	
215 220 225	
gcc ctg tct cag cct cgc gct atg ctg gaa gaa gga gaa gac ttg cag	838
Ala Leu Ser Gln Pro Arg Ala Met Leu Glu Glu Gly Glu Asp Leu Gln	
230 235 240	
tgc tgt atg atc tgc gtg gct cgc cgc gtg act gcg cca ttc cca tcc	886
Cys Cys Met Ile Cys Val Ala Arg Arg Val Thr Ala Pro Phe Pro Ser	
245 250 255	
agt cct gag agc ttt att acc aga cat gac ctt tcc gga aag gtt gtc	934
Ser Pro Glu Ser Phe Ile Thr Arg His Asp Leu Ser Gly Lys Val Val	
260 265 270 275	
aat ata gat aca aac tca ctt aga tct tcc atg agg cct ggc ttt gaa	982
Asn Ile Asp Thr Asn Ser Leu Arg Ser Ser Met Arg Pro Gly Phe Glu	
280 285 290	
gac ata atc cga aga tgt atc cag agg ttc ttc agt ctg aat gat ggg	1030
Asp Ile Ile Arg Arg Cys Ile Gln Arg Phe Phe Ser Leu Asn Asp Gly	
295 300 305	
cag tca tgg tcc cag aag cgt cac tat caa gaa gct tat gtt cat ggc	1078
Gln Ser Trp Ser Gln Lys Arg His Tyr Gln Glu Ala Tyr Val His Gly	
310 315 320	
cac gca gag acc ccc gtg tat cgt ttc tcc ttg gct gat gga act att	1126
His Ala Glu Thr Pro Val Tyr Arg Phe Ser Leu Ala Asp Gly Thr Ile	
325 330 335	
gtg agt gcg cag aca aaa agc aaa ctc ttc cgc aat cct gta acg aat	1174

Val	Ser	Ala	Gln	Thr	Lys	Ser	Lys	Leu	Phe	Arg	Asn	Pro	Val	Thr	Asn		
340					345					350					355		
gat	cgt	cac	ggc	ttc	atc	tcg	acc	cac	ttt	ctt	cag	aga	gaa	cag	aat	1222	
Asp	Arg	His	Gly	Phe	Ile	Ser	Thr	His	Phe	Leu	Gln	Arg	Glu	Gln	Asn		
				360					365					370			
gga	tac	aga	cca	aac	cca	aat	ccc	gca	gga	caa	ggc	atc	cga	cct	cct	1270	
Gly	Tyr	Arg	Pro	Asn	Pro	Asn	Pro	Ala	Gly	Gln	Gly	Ile	Arg	Pro	Pro		
			375					380					385				
gca	gca	ggg	tgt	ggc	gtg	agc	atg	tct	cca	aat	cag	aat	gta	cag	atg	1318	
Ala	Ala	Gly	Cys	Gly	Val	Ser	Met	Ser	Pro	Asn	Gln	Asn	Val	Gln	Met		
		390					395					400					
atg	ggc	agc	cgg	acc	tat	ggc	gtg	cca	gac	ccc	agc	aac	aca	ggg	cag	1366	
Met	Gly	Ser	Arg	Thr	Tyr	Gly	Val	Pro	Asp	Pro	Ser	Asn	Thr	Gly	Gln		
	405					410					415						
atg	ggg	gga	gct	agg	tac	ggg	gct	tct	agt	agc	gta	gcc	tca	ctg	acg	1414	
Met	Gly	Gly	Ala	Arg	Tyr	Gly	Ala	Ser	Ser	Ser	Val	Ala	Ser	Leu	Thr		
	420				425					430					435		
cca	gga	caa	agc	cta	cag	tcg	cca	tct	tcc	tat	cag	aac	agc	agc	tat	1462	
Pro	Gly	Gln	Ser	Leu	Gln	Ser	Pro	Ser	Ser	Tyr	Gln	Asn	Ser	Ser	Tyr		
				440					445					450			
ggg	ctc	agc	atg	agc	agt	ccc	ccc	cac	ggc	agt	cct	ggg	ctt	ggg	ccc	1510	
Gly	Leu	Ser	Met	Ser	Ser	Pro	Pro	His	Gly	Ser	Pro	Gly	Leu	Gly	Pro		
			455					460					465				
aac	cag	cag	aac	atc	atg	att	tcc	cct	cgg	aat	cgt	ggc	agc	cca	aag	1558	
Asn	Gln	Gln	Asn	Ile	Met	Ile	Ser	Pro	Arg	Asn	Arg	Gly	Ser	Pro	Lys		
		470					475					480					
atg	gcc	tcc	cac	cag	ttc	tct	cct	gct	gca	ggg	gca	cac	tca	ccc	atg	1606	
Met	Ala	Ser	His	Gln	Phe	Ser	Pro	Ala	Ala	Gly	Ala	His	Ser	Pro	Met		
	485					490					495						
gga	cct	tct	ggc	aac	aca	ggg	agc	cac	agc	ttt	tct	agc	agc	tcc	ctc	1654	
Gly	Pro	Ser	Gly	Asn	Thr	Gly	Ser	His	Ser	Phe	Ser	Ser	Ser	Ser	Leu		
	500				505					510					515		
agt	gcc	ttg	caa	gcc	atc	agt	gaa	ggc	gtg	ggg	acc	tct	ctt	tta	tct	1702	
Ser	Ala	Leu	Gln	Ala	Ile	Ser	Glu	Gly	Val	Gly	Thr	Ser	Leu	Leu	Ser		
				520					525					530			
act	ctg	tcc	tca	cca	ggc	ccc	aaa	ctg	gat	aat	tct	ccc	aat	atg	aat	1750	
Thr	Leu	Ser	Ser	Pro	Gly	Pro	Lys	Leu	Asp	Asn	Ser	Pro	Asn	Met	Asn		
			535					540					545				
ata	agc	cag	cca	agt	aaa	gtg	agt	ggg	cag	gac	tct	aag	agc	ccc	cta	1798	
Ile	Ser	Gln	Pro	Ser	Lys	Val	Ser	Gly	Gln	Asp	Ser	Lys	Ser	Pro	Leu		
		550					555					560					
ggc	tta	tac	tgt	gaa	cag	aat	cca	gtg	gag	agt	tca	gtg	tgt	cag	tca	1846	
Gly	Leu	Tyr	Cys	Glu	Gln	Asn	Pro	Val	Glu	Ser	Ser	Val	Cys	Gln	Ser		

565	570	575	
aac agc aga gat cac cca agt gaa aaa gaa agc aag gag agc agt ggg			1894
Asn Ser Arg Asp His Pro Ser Glu Lys Glu Ser Lys Glu Ser Ser Gly			
580	585	590	595
gag gtg tca gag acg ccc agg gga cct ctg gaa agc aaa ggc cac aag			1942
Glu Val Ser Glu Thr Pro Arg Gly Pro Leu Glu Ser Lys Gly His Lys			
600	605		610
aaa ctg ctg cag tta ctc acg tgc tcc tcc gac gac cga ggc cat tcc			1990
Lys Leu Leu Gln Leu Leu Thr Cys Ser Ser Asp Asp Arg Gly His Ser			
615	620		625
tcc ttg acc aac tct ccc ctg gat cca aac tgc aaa gac tct tcc gtt			2038
Ser Leu Thr Asn Ser Pro Leu Asp Pro Asn Cys Lys Asp Ser Ser Val			
630	635		640
agt gtc acc agc ccc tct gga gtg tcc tcc tca aca tca ggg aca gtg			2086
Ser Val Thr Ser Pro Ser Gly Val Ser Ser Ser Thr Ser Gly Thr Val			
645	650		655
tct tcc acc tcc aat gtg cat ggg tct ctg ttg caa gag aaa cac cgg			2134
Ser Ser Thr Ser Asn Val His Gly Ser Leu Leu Gln Glu Lys His Arg			
660	665		670
att ttg cac aag ttg ctg cag aat ggc aac tcc cca gcg gag gtc gcc			2182
Ile Leu His Lys Leu Leu Gln Asn Gly Asn Ser Pro Ala Glu Val Ala			
680	685		690
aag atc act gca gag gcc act ggg aag gac acg agc agc act gct tcc			2230
Lys Ile Thr Ala Glu Ala Thr Gly Lys Asp Thr Ser Ser Thr Ala Ser			
695	700		705
tgt gga gag ggg aca acc agg cag gag cag ctg agt cct aag aag aag			2278
Cys Gly Glu Gly Thr Thr Arg Gln Glu Gln Leu Ser Pro Lys Lys Lys			
710	715		720
gag aat aat gct ctg ctt aga tac ctg ctg gac agg gat gac ccc agt			2326
Glu Asn Asn Ala Leu Leu Arg Tyr Leu Leu Asp Arg Asp Asp Pro Ser			
725	730		735
gat gtg ctt gcc aaa gag ctg cag ccc cag gcc gac agt ggg gac agt			2374
Asp Val Leu Ala Lys Glu Leu Gln Pro Gln Ala Asp Ser Gly Asp Ser			
740	745		750
aaa ctg agt cag tgc agc tgc tcc acc aat ccc agc tct ggc caa gag			2422
Lys Leu Ser Gln Cys Ser Cys Ser Thr Asn Pro Ser Ser Gly Gln Glu			
760	765		770
aaa gac ccc aaa att aag acc gag acg aac gag gag gta tcg gga gac			2470
Lys Asp Pro Lys Ile Lys Thr Glu Thr Asn Glu Glu Val Ser Gly Asp			
775	780		785
ctg gat aat cta gat gcc att ctt gga gat ttg acc agt tct gac ttc			2518
Leu Asp Asn Leu Asp Ala Ile Leu Gly Asp Leu Thr Ser Ser Asp Phe			
790	795		800

tac aac aat cct aca aat ggc ggt cac cca ggg gcc aaa cag cag atg	2566
Tyr Asn Asn Pro Thr Asn Gly Gly His Pro Gly Ala Lys Gln Gln Met	
805 810 815	
ttt gca gga ccg agt tct ctg ggt ttg cga agt cca cag cct gtg cag	2614
Phe Ala Gly Pro Ser Ser Leu Gly Leu Arg Ser Pro Gln Pro Val Gln	
820 825 830 835	
tct gtt cgt cct cca tat aac cga gcg gtg tct ctg gat agc cct gtg	2662
Ser Val Arg Pro Pro Tyr Asn Arg Ala Val Ser Leu Asp Ser Pro Val	
840 845 850	
tct gtt ggc tca ggt ccg cca gtg aag aat gtc agt gct ttc cct ggg	2710
Ser Val Gly Ser Gly Pro Pro Val Lys Asn Val Ser Ala Phe Pro Gly	
855 860 865	
tta cca aaa cag ccc ata ctg gct ggg aat cca aga atg atg gat agt	2758
Leu Pro Lys Gln Pro Ile Leu Ala Gly Asn Pro Arg Met Met Asp Ser	
870 875 880	
cag gag aat tac ggt gcc aac atg ggc cca aac aga aat gtt cct gtg	2806
Gln Glu Asn Tyr Gly Ala Asn Met Gly Pro Asn Arg Asn Val Pro Val	
885 890 895	
aat ccg act tcc tcc ccc gga gac tgg ggc tta gct aac tca agg gcc	2854
Asn Pro Thr Ser Ser Pro Gly Asp Trp Gly Leu Ala Asn Ser Arg Ala	
900 905 910 915	
agc aga atg gag cct ctg gca tca agt ccc ctg gga aga act gga gcc	2902
Ser Arg Met Glu Pro Leu Ala Ser Ser Pro Leu Gly Arg Thr Gly Ala	
920 925 930	
gat tac agt gcc act tta ccc aga cct gcc atg ggg ggc tct gtg cct	2950
Asp Tyr Ser Ala Thr Leu Pro Arg Pro Ala Met Gly Gly Ser Val Pro	
935 940 945	
acc ttg cca ctt cgt tct aat cga ctg cca ggt gca aga cca tcg ttg	2998
Thr Leu Pro Leu Arg Ser Asn Arg Leu Pro Gly Ala Arg Pro Ser Leu	
950 955 960	
cag caa cag cag cag caa cag cag caa cag caa caa cag cag caa	3046
Gln Gln Gln Gln Gln Gln Gln Gln Gln Gln Gln Gln Gln Gln Gln	
965 970 975	
cag cag cag caa cag cag cag cag caa cag cag cag atg ctt caa atg	3094
Gln Gln Gln Gln Gln Gln Gln Gln Gln Gln Gln Gln Met Leu Gln Met	
980 985 990 995	
aga act ggt gag att ccc atg gga atg gga gtc aat ccc tat agc cca	3142
Arg Thr Gly Glu Ile Pro Met Gly Met Gly Val Asn Pro Tyr Ser Pro	
1000 1005 1010	
gca gtg ccg tct aac caa cca ggt tcc tgg cca gag ggc atg ctc tct	3190
Ala Val Pro Ser Asn Gln Pro Gly Ser Trp Pro Glu Gly Met Leu Ser	
1015 1020 1025	

atg gaa caa ggt cct cac ggg tct caa aat agg cct ctt ctt aga aac	3238
Met Glu Gln Gly Pro His Gly Ser Gln Asn Arg Pro Leu Leu Arg Asn	
1030 1035 1040	
tct ctg gat gat ctg ctt ggg cca cct tct aac gca gag ggc cag agt	3286
Ser Leu Asp Asp Leu Leu Gly Pro Pro Ser Asn Ala Glu Gly Gln Ser	
1045 1050 1055	
gac gag aga gct ctg ctg gac cag ctg cac aca ctc ctg agc aac aca	3334
Asp Glu Arg Ala Leu Leu Asp Gln Leu His Thr Leu Leu Ser Asn Thr	
1060 1065 1070 1075	
gat gcc aca ggt ctg gag gag atc gac agg gcc ttg gga att cct gag	3382
Asp Ala Thr Gly Leu Glu Glu Ile Asp Arg Ala Leu Gly Ile Pro Glu	
1080 1085 1090	
ctc gtg aat cag gga caa gct ttg gag tcc aaa cag gat gtt ttc caa	3430
Leu Val Asn Gln Gly Gln Ala Leu Glu Ser Lys Gln Asp Val Phe Gln	
1095 1100 1105	
ggc caa gaa gca gca gta atg atg gat cag aag gct gca cta tat gga	3478
Gly Gln Glu Ala Ala Val Met Met Asp Gln Lys Ala Ala Leu Tyr Gly	
1110 1115 1120	
cag aca tac cca gct cag ggt cct ccc ctt caa gga ggc ttt aac ctt	3526
Gln Thr Tyr Pro Ala Gln Gly Pro Pro Leu Gln Gly Gly Phe Asn Leu	
1125 1130 1135	
cag gga cag tca cca tcg ttt aac tct atg atg ggt cag att agc cag	3574
Gln Gly Gln Ser Pro Ser Phe Asn Ser Met Met Gly Gln Ile Ser Gln	
1140 1145 1150 1155	
caa ggc agc ttt cct ctg caa ggc atg cat cct aga gcc ggc ctc gtg	3622
Gln Gly Ser Phe Pro Leu Gln Gly Met His Pro Arg Ala Gly Leu Val	
1160 1165 1170	
aga cca agg acc aac acc ccg aag cag ctg aga atg cag ctt cag cag	3670
Arg Pro Arg Thr Asn Thr Pro Lys Gln Leu Arg Met Gln Leu Gln Gln	
1175 1180 1185	
agg cta cag ggc cag cag ttt tta aat cag agc cgg cag gca ctt gaa	3718
Arg Leu Gln Gly Gln Gln Phe Leu Asn Gln Ser Arg Gln Ala Leu Glu	
1190 1195 1200	
atg aaa atg gag aac cct gct ggc act gct gtg atg agg ccc atg atg	3766
Met Lys Met Glu Asn Pro Ala Gly Thr Ala Val Met Arg Pro Met Met	
1205 1210 1215	
ccc cag gct ttc ttt aat gcc caa atg gct gcc cag cag aaa cga gag	3814
Pro Gln Ala Phe Phe Asn Ala Gln Met Ala Ala Gln Gln Lys Arg Glu	
1220 1225 1230 1235	
ctg atg agc cat cac ctg cag cag cag agg atg gcg atg atg atg tca	3862
Leu Met Ser His His Leu Gln Gln Gln Arg Met Ala Met Met Met Ser	
1240 1245 1250	
caa cca cag cct cag gcc ttc agc cca cct ccc aac gtc acc gcc tcc	3910

Gln Pro Gln Pro Gln Ala Phe Ser Pro Pro Pro Asn Val Thr Ala Ser
1255 1260 1265

ccc agc atg gac ggg gtt ttg gca ggt tca gca atg ccg caa gcc cct 3958
Pro Ser Met Asp Gly Val Leu Ala Gly Ser Ala Met Pro Gln Ala Pro
1270 1275 1280

cca caa cag ttt cca tat cca gca aat tac gga atg gga caa cca cca 4006
Pro Gln Gln Phe Pro Tyr Pro Ala Asn Tyr Gly Met Gly Gln Pro Pro
1285 1290 1295

gag cca gcc ttt ggt cga ggc tcg agt cct ccc agt gca atg atg tca 4054
Glu Pro Ala Phe Gly Arg Gly Ser Ser Pro Pro Ser Ala Met Met Ser
1300 1305 1310 1315

tca aga atg ggg cct tcc cag aat gcc atg gtg cag cat cct cag ccc 4102
Ser Arg Met Gly Pro Ser Gln Asn Ala Met Val Gln His Pro Gln Pro
1320 1325 1330

aca ccc atg tat cag cct tca gat atg aag ggg tgg ccg tca ggg aac 4150
Thr Pro Met Tyr Gln Pro Ser Asp Met Lys Gly Trp Pro Ser Gly Asn
1335 1340 1345

ctg gcc agg aat ggc tcc ttc ccc cag cag cag ttt gct ccc cag ggg 4198
Leu Ala Arg Asn Gly Ser Phe Pro Gln Gln Gln Phe Ala Pro Gln Gly
1350 1355 1360

aac cct gca gcc tac aac atg gtg cat atg aac agc agc ggt ggg cac 4246
Asn Pro Ala Ala Tyr Asn Met Val His Met Asn Ser Ser Gly Gly His
1365 1370 1375

ttg gga cag atg gcc atg acc ccc atg ccc atg tct ggc atg ccc atg 4294
Leu Gly Gln Met Ala Met Thr Pro Met Pro Met Ser Gly Met Pro Met
1380 1385 1390 1395

ggc ccc gat cag aaa tac tgc tga catctcccta gtgggactga ctgtacagat 4348
Gly Pro Asp Gln Lys Tyr Cys
1400

gacactgcac aggatcatca ggacgtggcg gcgagtcatt gtctaagcat ccagcttgga 4408

aacaaggcca gcgtgaccag cagcgggggtc tgtgctgtca tttgagcaga gctgggtctc 4468

gctgaagcgc actgtctacc tgatgccttg cctctgtgtg gcaaggtgtt ctgcctcatg 4528

aggatgtgat tctggagatg ggggtgttcgt aagcaccgct ctcttaacgtc actcccttct 4588

gcctcgccag ccaaagtctt cacgtagatc tag 4621

<210> 10

<211> 22

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: forward primer

AlB1/mESTF1 to screen mouse BAC

<400> 10

tccttttccc agcagcagtt tg

22

<210> 11

<211> 20

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: reverse primer

AlB1/mESTR1 used to screen mouse BAC

<400> 11

atgccagaca tgggcatggg

20

<210> 12

<211> 1402

<212> PRT

<213> Mus musculus

<400> 12

Met Ser Gly Leu Gly Glu Ser Ser Leu Asp Pro Leu Ala Ala Glu Ser
1 5 10 15

Arg Lys Arg Lys Leu Pro Cys Asp Ala Pro Gly Gln Gly Leu Val Tyr
20 25 30

Ser Gly Glu Lys Trp Arg Arg Glu Gln Glu Ser Lys Tyr Ile Glu Glu
35 40 45

Leu Ala Glu Leu Ile Ser Ala Asn Leu Ser Asp Ile Asp Asn Phe Asn
50 55 60

Val Lys Pro Asp Lys Cys Ala Ile Leu Lys Glu Thr Val Arg Gln Ile
65 70 75 80

Arg Gln Ile Lys Glu Gln Gly Lys Thr Ile Ser Ser Asp Asp Asp Val
85 90 95

Gln Lys Ala Asp Val Ser Ser Thr Gly Gln Gly Val Ile Asp Lys Asp
100 105 110

Ser Leu Gly Pro Leu Leu Leu Gln Ala Leu Asp Gly Phe Leu Phe Val
115 120 125

Val Asn Arg Asp Gly Asn Ile Val Phe Val Ser Glu Asn Val Thr Gln
130 135 140

Tyr Leu Gln Tyr Lys Gln Glu Asp Leu Val Asn Thr Ser Val Tyr Ser
145 150 155 160

Ile Leu His Glu Gln Asp Arg Lys Asp Phe Leu Lys His Leu Pro Lys
165 170 175

Ser	Thr	Val	Asn	Gly	Val	Ser	Trp	Thr	Asn	Glu	Asn	Gln	Arg	Gln	Lys	180	185	190	
Ser	His	Thr	Phe	Asn	Cys	Arg	Met	Leu	Met	Lys	Thr	His	Asp	Ile	Leu	195	200	205	
Glu	Asp	Val	Asn	Ala	Ser	Pro	Glu	Thr	Arg	Gln	Arg	Tyr	Glu	Thr	Met	210	215	220	
Gln	Cys	Phe	Ala	Leu	Ser	Gln	Pro	Arg	Ala	Met	Leu	Glu	Glu	Gly	Glu	225	230	235	240
Asp	Leu	Gln	Cys	Cys	Met	Ile	Cys	Val	Ala	Arg	Arg	Val	Thr	Ala	Pro	245	250	255	
Phe	Pro	Ser	Ser	Pro	Glu	Ser	Phe	Ile	Thr	Arg	His	Asp	Leu	Ser	Gly	260	265	270	
Lys	Val	Val	Asn	Ile	Asp	Thr	Asn	Ser	Leu	Arg	Ser	Ser	Met	Arg	Pro	275	280	285	
Gly	Phe	Glu	Asp	Ile	Ile	Arg	Arg	Cys	Ile	Gln	Arg	Phe	Phe	Ser	Leu	290	295	300	
Asn	Asp	Gly	Gln	Ser	Trp	Ser	Gln	Lys	Arg	His	Tyr	Gln	Glu	Ala	Tyr	305	310	315	320
Val	His	Gly	His	Ala	Glu	Thr	Pro	Val	Tyr	Arg	Phe	Ser	Leu	Ala	Asp	325	330	335	
Gly	Thr	Ile	Val	Ser	Ala	Gln	Thr	Lys	Ser	Lys	Leu	Phe	Arg	Asn	Pro	340	345	350	
Val	Thr	Asn	Asp	Arg	His	Gly	Phe	Ile	Ser	Thr	His	Phe	Leu	Gln	Arg	355	360	365	
Glu	Gln	Asn	Gly	Tyr	Arg	Pro	Asn	Pro	Asn	Pro	Ala	Gly	Gln	Gly	Ile	370	375	380	
Arg	Pro	Pro	Ala	Ala	Gly	Cys	Gly	Val	Ser	Met	Ser	Pro	Asn	Gln	Asn	385	390	395	400
Val	Gln	Met	Met	Gly	Ser	Arg	Thr	Tyr	Gly	Val	Pro	Asp	Pro	Ser	Asn	405	410	415	
Thr	Gly	Gln	Met	Gly	Gly	Ala	Arg	Tyr	Gly	Ala	Ser	Ser	Ser	Val	Ala	420	425	430	
Ser	Leu	Thr	Pro	Gly	Gln	Ser	Leu	Gln	Ser	Pro	Ser	Ser	Tyr	Gln	Asn	435	440	445	
Ser	Ser	Tyr	Gly	Leu	Ser	Met	Ser	Ser	Pro	Pro	His	Gly	Ser	Pro	Gly	450	455	460	
Leu	Gly	Pro	Asn	Gln	Gln	Asn	Ile	Met	Ile	Ser	Pro	Arg	Asn	Arg	Gly	465	470	475	480

Ser	Pro	Lys	Met	Ala	Ser	His	Gln	Phe	Ser	Pro	Ala	Ala	Gly	Ala	His	485	490	495
Ser	Pro	Met	Gly	Pro	Ser	Gly	Asn	Thr	Gly	Ser	His	Ser	Phe	Ser	Ser	500	505	510
Ser	Ser	Leu	Ser	Ala	Leu	Gln	Ala	Ile	Ser	Glu	Gly	Val	Gly	Thr	Ser	515	520	525
Leu	Leu	Ser	Thr	Leu	Ser	Ser	Pro	Gly	Pro	Lys	Leu	Asp	Asn	Ser	Pro	530	535	540
Asn	Met	Asn	Ile	Ser	Gln	Pro	Ser	Lys	Val	Ser	Gly	Gln	Asp	Ser	Lys	545	550	555
Ser	Pro	Leu	Gly	Leu	Tyr	Cys	Glu	Gln	Asn	Pro	Val	Glu	Ser	Ser	Val	565	570	575
Cys	Gln	Ser	Asn	Ser	Arg	Asp	His	Pro	Ser	Glu	Lys	Glu	Ser	Lys	Glu	580	585	590
Ser	Ser	Gly	Glu	Val	Ser	Glu	Thr	Pro	Arg	Gly	Pro	Leu	Glu	Ser	Lys	595	600	605
Gly	His	Lys	Lys	Leu	Leu	Gln	Leu	Leu	Thr	Cys	Ser	Ser	Asp	Asp	Arg	610	615	620
Gly	His	Ser	Ser	Leu	Thr	Asn	Ser	Pro	Leu	Asp	Pro	Asn	Cys	Lys	Asp	625	630	635
Ser	Ser	Val	Ser	Val	Thr	Ser	Pro	Ser	Gly	Val	Ser	Ser	Ser	Thr	Ser	645	650	655
Gly	Thr	Val	Ser	Ser	Thr	Ser	Asn	Val	His	Gly	Ser	Leu	Leu	Gln	Glu	660	665	670
Lys	His	Arg	Ile	Leu	His	Lys	Leu	Leu	Gln	Asn	Gly	Asn	Ser	Pro	Ala	675	680	685
Glu	Val	Ala	Lys	Ile	Thr	Ala	Glu	Ala	Thr	Gly	Lys	Asp	Thr	Ser	Ser	690	695	700
Thr	Ala	Ser	Cys	Gly	Glu	Gly	Thr	Thr	Arg	Gln	Glu	Gln	Leu	Ser	Pro	705	710	715
Lys	Lys	Lys	Glu	Asn	Asn	Ala	Leu	Leu	Arg	Tyr	Leu	Leu	Asp	Arg	Asp	725	730	735
Asp	Pro	Ser	Asp	Val	Leu	Ala	Lys	Glu	Leu	Gln	Pro	Gln	Ala	Asp	Ser	740	745	750
Gly	Asp	Ser	Lys	Leu	Ser	Gln	Cys	Ser	Cys	Ser	Thr	Asn	Pro	Ser	Ser	755	760	765
Gly	Gln	Glu	Lys	Asp	Pro	Lys	Ile	Lys	Thr	Glu	Thr	Asn	Glu	Glu	Val	770	775	780

Ser Gly Asp Leu Asp Asn Leu Asp Ala Ile Leu Gly Asp Leu Thr Ser
 785 790 795 800
 Ser Asp Phe Tyr Asn Asn Pro Thr Asn Gly Gly His Pro Gly Ala Lys
 805 810 815
 Gln Gln Met Phe Ala Gly Pro Ser Ser Leu Gly Leu Arg Ser Pro Gln
 820 825 830
 Pro Val Gln Ser Val Arg Pro Pro Tyr Asn Arg Ala Val Ser Leu Asp
 835 840 845
 Ser Pro Val Ser Val Gly Ser Gly Pro Pro Val Lys Asn Val Ser Ala
 850 855 860
 Phe Pro Gly Leu Pro Lys Gln Pro Ile Leu Ala Gly Asn Pro Arg Met
 865 870 875 880
 Met Asp Ser Gln Glu Asn Tyr Gly Ala Asn Met Gly Pro Asn Arg Asn
 885 890 895
 Val Pro Val Asn Pro Thr Ser Ser Pro Gly Asp Trp Gly Leu Ala Asn
 900 905 910
 Ser Arg Ala Ser Arg Met Glu Pro Leu Ala Ser Ser Pro Leu Gly Arg
 915 920 925
 Thr Gly Ala Asp Tyr Ser Ala Thr Leu Pro Arg Pro Ala Met Gly Gly
 930 935 940
 Ser Val Pro Thr Leu Pro Leu Arg Ser Asn Arg Leu Pro Gly Ala Arg
 945 950 955 960
 Pro Ser Leu Gln Gln Gln Gln Gln Gln Gln Gln Gln Gln Gln Gln
 965 970 975
 Gln Gln Gln Gln Gln Gln Gln Gln Gln Gln Gln Gln Gln Gln Met
 980 985 990
 Leu Gln Met Arg Thr Gly Glu Ile Pro Met Gly Met Gly Val Asn Pro
 995 1000 1005
 Tyr Ser Pro Ala Val Pro Ser Asn Gln Pro Gly Ser Trp Pro Glu Gly
 1010 1015 1020
 Met Leu Ser Met Glu Gln Gly Pro His Gly Ser Gln Asn Arg Pro Leu
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 Leu Arg Asn Ser Leu Asp Asp Leu Leu Gly Pro Pro Ser Asn Ala Glu
 1045 1050 1055
 Gly Gln Ser Asp Glu Arg Ala Leu Leu Asp Gln Leu His Thr Leu Leu
 1060 1065 1070
 Ser Asn Thr Asp Ala Thr Gly Leu Glu Glu Ile Asp Arg Ala Leu Gly
 1075 1080 1085

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Ile Pro Glu Leu Val Asn Gln Gly Gln Ala Leu Glu Ser Lys Gln Asp
 1090 1095 1100
 Val Phe Gln Gly Gln Glu Ala Ala Val Met Met Asp Gln Lys Ala Ala
 1105 1110 1115 1120
 Leu Tyr Gly Gln Thr Tyr Pro Ala Gln Gly Pro Pro Leu Gln Gly Gly
 1125 1130 1135
 Phe Asn Leu Gln Gly Gln Ser Pro Ser Phe Asn Ser Met Met Gly Gln
 1140 1145 1150
 Ile Ser Gln Gln Gly Ser Phe Pro Leu Gln Gly Met His Pro Arg Ala
 1155 1160 1165
 Gly Leu Val Arg Pro Arg Thr Asn Thr Pro Lys Gln Leu Arg Met Gln
 1170 1175 1180
 Leu Gln Gln Arg Leu Gln Gly Gln Gln Phe Leu Asn Gln Ser Arg Gln
 1185 1190 1195 1200
 Ala Leu Glu Met Lys Met Glu Asn Pro Ala Gly Thr Ala Val Met Arg
 1205 1210 1215
 Pro Met Met Pro Gln Ala Phe Phe Asn Ala Gln Met Ala Ala Gln Gln
 1220 1225 1230
 Lys Arg Glu Leu Met Ser His His Leu Gln Gln Gln Arg Met Ala Met
 1235 1240 1245
 Met Met Ser Gln Pro Gln Pro Gln Ala Phe Ser Pro Pro Pro Asn Val
 1250 1255 1260
 Thr Ala Ser Pro Ser Met Asp Gly Val Leu Ala Gly Ser Ala Met Pro
 1265 1270 1275 1280
 Gln Ala Pro Pro Gln Gln Phe Pro Tyr Pro Ala Asn Tyr Gly Met Gly
 1285 1290 1295
 Gln Pro Pro Glu Pro Ala Phe Gly Arg Gly Ser Ser Pro Pro Ser Ala
 1300 1305 1310
 Met Met Ser Ser Arg Met Gly Pro Ser Gln Asn Ala Met Val Gln His
 1315 1320 1325
 Pro Gln Pro Thr Pro Met Tyr Gln Pro Ser Asp Met Lys Gly Trp Pro
 1330 1335 1340
 Ser Gly Asn Leu Ala Arg Asn Gly Ser Phe Pro Gln Gln Gln Phe Ala
 1345 1350 1355 1360
 Pro Gln Gly Asn Pro Ala Ala Tyr Asn Met Val His Met Asn Ser Ser
 1365 1370 1375
 Gly Gly His Leu Gly Gln Met Ala Met Thr Pro Met Pro Met Ser Gly
 1380 1385 1390

Met Pro Met Gly Pro Asp Gln Lys Tyr Cys
1395 1400
